



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coughlin, Shaun  
Ishihari, Hiroaki  
Connolly, Andrew
- (ii) TITLE OF THE INVENTION: Protease Activated Receptor  
3 and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 Page Mill Road  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/208,629  
(B) FILING DATE: 08-DEC-1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/742,440  
(B) FILING DATE: 30-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Catherine M. Polizzi  
(B) REGISTRATION NUMBER: 40,130  
(C) REFERENCE/DOCKET NUMBER: 220002060310
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (650) 813-5600  
(B) TELEFAX: (650) 494-0792  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACATTATA	GAGTTTAAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTCTGT	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGATGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TCCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTT	CTCATCCCGT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
TCATCCTTGT	GATTTTCACA	ATTGCTTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTACTT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCCTTTA	CTTTGTCTAT	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1124  
(D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTTT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180
CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
GACCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCAA	300
CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCGG	TTTAAGATCN	NCCTACCATC	360
TCAATGGCAA	CAACTGGGTA	TTTGGCGAGG	TCATGTGCGG	GATCACCACG	GTCGTTTTCT	420
ACGGCAACAT	GTAATGCGCT	ANNNTCCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
TGGCCACGGC	TCACCCTTTC	ACATAACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
TGTGTGGCAT	GGTGTGGGCT	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600
CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCTGTCTCT	TAGCATTCTT	TGGGTTCTCT	720
ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCTCTA	TCCTTGTGAA	TTTACCACATC	840
TGCTTCCCCC	CCACCAAGNN	NNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960

TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
GGTTAGCCTT	GAAGTCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080
AGGTCCTGGCA	AGCGCTCCAT	TTTTCAGCTC	CTCTGCAACA	GTGC		1124

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu Tyr Thr

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCACTTT	TTGTCAGAGT	120
GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCGT	180
GGAGCTCCCC	CAAATTCCTT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
GCCACGATTA	CTGTAAAAAT	TAAGTGCCCT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
AGGACCAGAT	CCATCTGTAC	CACTGTATT	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480
TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTACCTAC	660
CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTCTAT	840
TACTTCATCT	CCTTGGCATT	CTTTGGATT	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTAAAG	960
GCGAGTCTCC	TCATCCTTGT	GATTTTTTACC	ATTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
ATTATTCACC	ATGCTAACTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCCTTTA	TTTTCTCATG	1140
TCAAAAACCA	GAAATCACTC	CACTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
TTCAGGACCA	GATCCATCTG	TACCACTGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
CTTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTACTGCTCC	480
ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCACC	540
TACCGGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
GTTTTCTTAT	ATATGCTGCC	ATTTTTCATA	CTGAAGCAGG	AATATTATCT	TGTTCAGCCA	660
GACATCACCA	CCTGCCATGA	TGTTCACAAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
TATTACTTCA	TCTCCTTGGC	ATTCTTTGGA	TTCTTAATTC	CATTTGTGCT	TATCATCTAC	780
TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTGTCT	TTGCTCCAAG	CAATATTATT	900
CTTATTATTC	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTTCCT	TTATTTTCTC	1020
ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys Ser Met Ile Leu Gln Ile Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Pro	Arg	Arg	Leu	Leu	Leu	Val	Ala	Ala	Cys	Phe	Ser	Leu	Cys
1				5				10						15	
Gly	Pro	Leu	Leu	Ser	Ala	Arg	Thr	Arg	Ala	Arg	Arg	Pro	Glu	Ser	Lys
		20						25					30		
Ala	Thr	Asn	Ala	Thr	Leu	Asp	Pro	Arg	Ser	Phe	Leu	Leu	Arg	Asn	Pro
		35					40					45			
Asn	Asp	Lys	Tyr	Glu	Pro	Phe	Trp	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Ser
	50					55				60					
Gly	Leu	Thr	Glu	Tyr	Arg	Leu	Val	Ser	Ile	Asn	Lys	Ser	Ser	Pro	Leu
65					70				75					80	
Gln	Lys	Gln	Leu	Pro	Ala	Phe	Ile	Ser	Glu	Asp	Ala	Ser	Gly	Tyr	Leu
			85					90					95		
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val
			100					105					110		

Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile	115	120	125
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu	130	135	140
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser	145	150	155
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg	165	170	175
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	180	185	190
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met	195	200	205
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu	210	215	220
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys	225	230	235
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	245	250	255
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser	260	265	270
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val	275	280	285
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn	290	295	300
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys	305	310	315
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His	325	330	335
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala	340	345	350
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro	355	360	365
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser	370	375	380
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser	385	390	395
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn	405	410	415
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr								420	425	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Arg	Ser	Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu	1	5	10	15
Ala	Ala	Ser	Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser	20	25	30	
Ser	Lys	Gly	Arg	Ser	Leu	Ile	Gly	Lys	Val	Asp	Gly	Thr	Ser	His	Val	35	40	45	
Thr	Gly	Lys	Gly	Val	Thr	Val	Glu	Thr	Val	Phe	Ser	Val	Asp	Glu	Phe				

50		55		60											
Ser	Ala	Ser	Val	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile
65				70						75					80
Val	Tyr	Thr	Ile	Val	Phe	Val	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala
			85						90					95	
Leu	Trp	Val	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile
		100						105					110		
Tyr	Met	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe
	115						120					125			
Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly
	130					135					140				
Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr
145				150						155					160
Cys	Ser	Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val
			165						170					175	
Ile	Val	Asn	Pro	Met	Gly	His	Ser	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Ile
		180						185					190		
Gly	Ile	Ser	Leu	Ala	Ile	Trp	Leu	Leu	Ile	Leu	Leu	Val	Thr	Ile	Pro
	195						200					205			
Leu	Tyr	Val	Val	Lys	Gln	Thr	Ile	Phe	Ile	Pro	Ala	Leu	Asn	Ile	Thr
	210					215					220				
Thr	Cys	His	Asp	Val	Leu	Pro	Glu	Gln	Leu	Leu	Val	Gly	Asp	Pro	Phe
225				230						235					240
Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Phe	Leu	Thr	Ala
			245						250					255	
Ser	Ala	Tyr	Val	Leu	Met	Ile	Arg	Met	Leu	Arg	Ser	Ser	Ala	Met	Asp
	260							265					270		
Glu	Asn	Ser	Glu	Lys	Lys	Arg	Lys	Arg	Ala	Ile	Lys	Leu	Ile	Val	Thr
	275						280					285			
Val	Leu	Ala	Met	Tyr	Leu	Ile	Cys	Phe	Thr	Pro	Ser	Asn	Leu	Leu	Leu
	290					295					300				
Val	Val	His	Tyr	Phe	Leu	Ile	Lys	Ser	Gln	Gly	Gln	Ser	His	Val	Tyr
305				310						315					320
Ala	Leu	Tyr	Ile	Val	Ala	Leu	Cys	Leu	Ser	Thr	Leu	Asn	Ser	Cys	Ile
			325						330					335	
Asp	Pro	Phe	Val	Tyr	Tyr	Phe	Val	Ser	His	Asp	Phe	Arg	Asp	His	Ala
		340						345					350		
Lys	Asn	Ala	Leu	Leu	Cys	Arg	Ser	Val	Arg	Thr	Val	Lys	Gln	Met	Gln
	355					360						365			
Val	Ser	Leu	Thr	Ser	Lys	Lys	His	Ser	Arg	Lys	Ser	Ser	Ser	Tyr	Ser
	370				375						380				
Ser	Ser	Ser	Thr	Thr	Val	Lys	Thr	Ser	Tyr						
385				390											

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp	Phe	Glu	Glu	Ile	Pro	Glu	Glu	Tyr	Leu	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKNTC

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp

1

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
 1              5              10              15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
      20              25              30
Lys Asp Asp Asp Asp Val Glu
      35
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Phe Glu Glu Phe Pro
 1              5
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Leu Thr Pro Lys
 1
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu  
1 5 10 15  
Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu  
1 5 10 15  
Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu  
1 5 10 15  
Glu Phe Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe  
1 5 10 15  
Pro Phe Ser Ala Leu Glu  
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys  
1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

Gln	His	Pro	Val	Ala	Gly	Ser	Gln	Asp	Ile	Lys	Met	Lys	Ile	Leu	Ile
1				5					10					15	
Leu	Val	Ala	Ala	Gly	Leu	Leu	Phe	Leu	Pro	Val	Thr	Val	Cys	Gln	Ser
			20					25					30		
Gly	Ile	Asn	Val	Ser	Asp	Asn	Ser	Ala	Lys	Pro	Thr	Leu	Thr	Ile	Lys
		35				40						45			
Ser	Phe	Asn	Gly	Gly	Pro	Gln	Asn	Thr	Phe	Glu	Glu	Phe	Pro	Leu	Ser
	50					55				60					
Asp	Ile	Glu	Gly	Trp	Thr	Gly	Ala	Thr	Thr	Thr	Ile	Lys	Ala	Glu	Cys
65					70					75					80
Pro	Glu	Asp	Ser	Ile	Ser	Thr	Leu	His	Val	Asn	Asn	Ala	Thr	Ile	Gly
			85						90					95	
Tyr	Leu	Arg	Ser	Ser	Leu	Ser	Thr	Gln	Val	Ile	Pro	Ala	Ile	Tyr	Ile
			100					105						110	
Leu	Leu	Phe	Val	Val	Gly	Val	Pro	Ser	Asn	Ile	Val	Thr	Leu	Trp	Lys
		115					120					125			
Leu	Ser	Leu	Arg	Thr	Lys	Ser	Ile	Ser	Leu	Val	Ile	Phe	His	Thr	Asn
	130					135						140			
Leu	Ala	Ile	Ala	Asp	Leu	Leu	Phe	Cys	Val	Thr	Leu	Pro	Phe	Lys	Ile
145					150					155					160
Ala	Tyr	His	Leu	Asn	Gly	Asn	Asn	Trp	Val	Phe	Gly	Glu	Val	Met	Cys
			165						170					175	
Arg	Ile	Thr	Thr	Val	Val	Phe	Tyr	Gly	Asn	Met	Tyr	Cys	Ala	Ile	Leu
			180					185						190	
Ile	Leu	Thr	Cys	Met	Gly	Ile	Asn	Arg	Tyr	Leu	Ala	Thr	Ala	His	Pro
		195					200					205			
Phe	Thr	Tyr	Gln	Lys	Leu	Pro	Lys	Arg	Ser	Phe	Ser	Leu	Leu	Met	Cys
	210					215					220				
Gly	Ile	Val	Trp	Val	Met	Val	Phe	Leu	Tyr	Met	Leu	Pro	Phe	Val	Ile
225					230					235					240
Leu	Lys	Gln	Glu	Tyr	His	Leu	Val	His	Ser	Glu	Ile	Thr	Thr	Cys	His
			245						250					255	
Asp	Val	Val	Asp	Ala	Cys	Glu	Ser	Pro	Ser	Ser	Phe	Arg	Phe	Tyr	Tyr
			260					265					270		
Phe	Val	Ser	Leu	Ala	Phe	Phe	Gly	Phe	Leu	Ile	Pro	Phe	Val	Ile	Ile
		275					280					285			
Ile	Phe	Cys	Tyr	Thr	Thr	Leu	Ile	His	Lys	Leu	Lys	Ser	Lys	Asp	Arg
	290					295					300				
Ile	Trp	Leu	Gly	Tyr	Ile	Lys	Ala	Val	Leu	Leu	Ile	Leu	Val	Ile	Phe
305					310					315					320
Thr	Ile	Cys	Phe	Ala	Pro	Thr	Asn	Ile	Ile	Leu	Val	Ile	His	His	Ala
			325						330					335	
Asn	Tyr	Tyr	Tyr	His	Asn	Thr	Asp	Ser	Leu	Tyr	Phe	Met	Tyr	Leu	Ile
			340					345					350		
Ala	Leu	Cys	Leu	Gly	Ser	Leu	Asn	Ser	Cys	Leu	Asp	Pro	Phe	Leu	Tyr
		355					360					365			
Phe	Val	Met	Ser	Lys	Val	Val	Asp	Gln	Leu	Asn	Pro				
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

Ser Ala Met Ala Arg Pro Leu

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Arg Pro Arg Arg Asp Ile Trp Glu Asp Ile His Ala Trp

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10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Cys Ser Met Ile Leu Gln Ile Ser Xaa Arg Leu Arg Asp Gly Thr Gln  
1 5 10 15  
Val Ile Lys Met Lys Ala Leu Ile Phe Ala Ala Ala Gly Leu Leu Leu  
20 25 30  
Leu Leu Pro Thr Phe Cys Gln Ser Gly Met Glu Asn Asp Thr Asn Asn  
35 40 45  
Leu Ala Lys Pro Thr Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro  
50 55 60  
Asn Ser Phe Glu Glu Phe Pro Phe Ser Ala Leu Glu Gly Trp Thr Gly  
65 70 75 80  
Ala Thr Ile Thr Val Lys Ile Lys Cys Pro Glu Glu Ser Ala Ser His  
85 90 95  
Leu His Val Lys Asn Ala Thr Met Gly Tyr Leu Thr Ser Ser Leu Ser  
100 105 110  
Thr Lys Leu Ile Pro Ala Ile Tyr Leu Leu Val Phe Val Val Gly Val  
115 120 125  
Pro Ala Asn Ala Val Thr Leu Trp Met Leu Phe Phe Arg Thr Arg Ser  
130 135 140  
Ile Cys Thr Thr Val Phe Tyr Thr Asn Leu Ala Ile Ala Asp Phe Leu  
145 150 155 160  
Phe Cys Val Thr Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn  
165 170 175  
Asn Trp Val Phe Gly Glu Val Leu Cys Arg Ala Thr Thr Val Ile Phe  
180 185 190  
Tyr Gly Asn Met Tyr Cys Ser Ile Leu Leu Leu Ala Cys Ile Ser Ile  
195 200 205  
Asn Arg Tyr Leu Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro  
210 215 220  
Lys His Thr Tyr Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val  
225 230 235 240  
Phe Leu Tyr Met Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu  
245 250 255  
Val Gln Pro Asp Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu  
260 265 270  
Ser Ser Ser Pro Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe  
275 280 285  
Gly Phe Leu Ile Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile

290                      295                      300  
 Ile Arg Thr Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys  
 305                      310                      315                      320  
 Ala Ser Leu Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser  
                     325                      330                      335  
 Asn Ile Ile Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr  
                     340                      345                      350  
 Asp Gly Leu Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu  
                     355                      360                      365  
 Asn Ser Cys Leu Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg  
                     370                      375                      380  
 Asn His Ser Thr Ala Tyr Leu Thr Lys  
                     385                      390

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

Asn Asp Leu Arg Glu Gln Gly Gln Pro Ser Gln Arg Thr  
 1                      5                      10